

GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 5, 2003, 01:52:07 ; Search time 3095 Seconds  
(without alignments)  
4137.394 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270

Sequence: 1 MSMSVALLWVSTSEVSNQ.....IYAKSLVPPNRTSSPLAKT 440

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14531402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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41: em\_htgo\_other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1827	80.5	1295	8 CAPSY1	X68017 C. annum ps
2	1751	77.1	1786	8 TOMCBPE	M84744 Tomato phyt
3	1750	77.1	1239	6 A68204	A68204 Sequence 2
4	1750	77.1	1239	6 AR156064	AR156064 Sequence
5	1750	77.1	1239	6 BD005486	BD005486 Enhance
6	1744	76.8	1239	6 A68203	A68203 Sequence 1
7	1744	76.8	1239	6 AR156063	AR156063 Sequence
8	1744	76.8	1239	6 BD005485	BD005485 Enhance
9	1733	76.3	1614	8 LER1PE	Y00521 Tomato fru
10	1732	76.3	1646	6 A21360	A21360 L. esculentu
11	1732	76.3	1646	6 AR007503	AR007503 Sequence
12	1668	73.5	1355	8 LERYCTOM5	X67144 L. esculentu
13	1626	71.6	1506	8 AF220218	AF220218 Citrus un
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15	1606	70.7	1773	8 AF152892	AF152892 Citrus x
16	1598	70.4	1637	8 HAN308385	AJ308385 Helianthu
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18	1590	70.0	1598	8 HAN304825	AJ304825 Helianthu
19	1580.5	69.6	1376	8 AY099482	AY099482 Tagetes e
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22	1559.5	68.7	1372	6 A48337	A48337 Sequence 1
23	1557	68.6	1921	6 E15681	E15681 Gentiana lu
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25	1542	67.9	1703	8 AY085565	AY085565 Arabidops
26	1531	67.4	2085	6 E15680	E15680 Gentiana lu
27	1530	67.4	1119	8 TOMPSY2A	L23424 Lycopersico
28	1526.5	67.2	1769	8 ATHPHYSYN	L25812 Arabidops
29	1523	67.1	1932	6 E15682	E15682 Gentiana lu
30	1519	66.9	1548	8 NPPSY	X78814 N. pseudonar
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32	1431.5	63.1	1304	6 AX350858	AX350858 Sequence
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34	1282.5	56.5	3707	8 LEGTOM5	X60441 L. esculentu
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36	1268.5	55.9	75188	8 AB005238	AB005238 Arabidops
37	1212	53.4	1060	8 AY024350	AY024350 Oryza sat
38	1064	46.9	681	8 AF196963	AF196963 Bixa orel
39	1059	46.7	686	8 AF158024	AF158024 Tagetes e
40	1054.5	46.5	1278	8 DBU91900	U91900 Dupaliella
41	1052	46.3	1859	8 AF305430	AF305430 Haematoco
42	1026.5	45.2	139380	2 CNS08CAG	AL831803 Oryza sat
43	1015	44.7	5995	8 ZMU032636	U32636 Zea mays ph
44	1010	44.5	3222	8 AY024351	AY024351 Oryza sat
45	901	39.7	1465	1 SSPPHYSYN	X69172 Synechocyst

# ALIGNMENTS

RESULT 1

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CAPSY1
LOCUS       CAPSY1               1295 bp    mRNA          linear    PLN 05-FEB-1994
DEFINITION  C.annuum psyl mRNA for phytoene synthase.
ACCESSION   X68017
VERSION     X68017.1 GI:433993
KEYWORDS    phytoene synthase.
SOURCE      Capsicum annuum.
ORGANISM    Capsicum annuum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridaceae; euasterids I; Solanales; Solanaceae; Capsicum.
REFERENCE   1 (bases 1 to 1295)
AUTHORS     Kuntz, M.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUL-1992) M. Kuntz, Inst. de Biologie Molec. des
            Plantes, 12 rue du Glirral Zimmer, 67084 Strasbourg, FRANCE
REFERENCE   2 (bases 1 to 1295)
AUTHORS     Romer, S., Huquaney, P., Bouvier, F., Camara, B. and Kuntz, M.
TITLE       Expression of the genes encoding the early carotenoid biosynthetic
            enzymes in Capsicum annuum
JOURNAL     Biochem. Biophys. Res. Commun. 196 (3), 1414-1421 (1993)
MEDLINE     94071905
PUBMED      8250898

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QY 102 SerSerGluLysValThrAspValValLeuLysGlnAlaAlaLeuValLysArgGln 121
262 TCATCAGAACGGATGTTATGATGATGTTTGGAGGAGCAGCCCTTGGTGAAGAGACAG 321
QY 122 LeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyLysLeuGly 141
322 CTGAGATCCACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 381
QY 142 LeuLeuSerGluAlaThrAspArgCysGlyGluValCysAlaGluThrAlaLysThrPhe 161
382 TTGTTGAGTGAAGCATATGATAGGTGTAGTAAGTATGTGCAGAGTACGCAACACGTTT 441
QY 162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrAlaIleThrVal 181
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502 TGGTCAGAGAGAACAGACGAACTTGTGATGTTGTCGCAATGCATCACACATTACTCCGGC 561
QY 202 AlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221
562 GCCTTAGATAGGTGGGAGACAGCGCTAGAGATGTTTTCAGTGGAGCGCCATTGACATG 621
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622 CTCGATGCTGTTTGTCCGACACAGTTTCCAAATTTCCAGTTTCATATTCAGCCATTTCGA 681
QY 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu 261
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QY 282 GlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
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QY 382 ValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyr 401
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QY 402 AsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIle 421
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QY 422 AlaTyrAlaLysSerLeuValProProAsnArgThr 433
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Db 1222 GCATATGCAAAATCTCTTGTCCTCTACAGACGA 1257

## RESULT 2

## TOMCBPE

LOCUS TOMCBPE 1786 bp mRNA linear PLN 27-APR-1993  
DEFINITION Tomato phytoene synthetase mRNA, complete cds.  
ACCESSION M84744  
VERSION M84744.1 GI:170415  
KEYWORDS carotenoid biosynthesis; phytoene synthetase.  
SOURCE Lycopersicon esculentum (library: Clontech fruit cDNA) breaker fruit stage fruit cDNA to mRNA.

## ORGANISM

Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.

## REFERENCE

1 (bases 1 to 1786) *Wang, L., Vanden, P. V., Bacot, K. O. and Scolnik, P. A., "A tomato gene expressed during fruit ripening encodes an enzyme of the carotenoid biosynthesis pathway"*  
J Biol Chem 267(8):5036-5039 (1992)

## JOURNAL

## MEDLINE

## PUBMED

## FEATURES

## source

1..1786 Location/Qualifiers

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polya\_site

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Score: 1751.00 Matches: 344

Percent Similarity: 86.67% Conservative: 33

Best Local Similarity: 79.08% Mismatches: 34

Query Match: 77.14% Indels: 24

DB: 8 Gaps: 3

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DB 365 ACAAGTTTCATGAATCAGTCGCGGAGGGAACCGGTTTTTTTGATTTCATCG----- 415

QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGlyGlyGlyGlyGly 60

DB 416 ---AGGCATAGGAATTTGGTGTCCATGAGAGAATCAATAGAGGT----- 457

QY 61 AsnPheGlySerLeuLeuAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80

DB 458 -----GGTGGAAAGCAAACTAAT 475

QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100  
DB 476 AATGACGGAATTTTCTGTCGGTCTCTATTTTGGCTACTCCATCTGGAGAAGCGAGC 535  
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QY 141 GlyLeuLeuSerGluAlaTrpAspArgCysGlyGluValCysAlaGluTrpAlaLysThr 160  
DB 656 GGCTGTGTTGAGTGAAGCATATGATAGTGTGTGAAGTATGTGCAGAGTATGCAAGAGC 715  
QY 161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaAlaIleTrpAlaIleTyr 180  
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QY 181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200  
DB 776 GTATGTCGAGAAGACAGATCACTGTTGATGGCCCAACGCATCATATATACCCCG 835  
QY 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgPropheAsp 220  
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QY 261 GluLeuTyrLeuTyrCysTyrTrpValAlaGlyThrValGlyLeuMetSerValProVal 280  
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QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300  
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DB 1316 AGAAAGTCTTTGATGAGCAGAGAAAGCGGTGACAGAAATTTGAGCTCAGCTAGTATTC 1375  
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RESULT 3

**A68204**  
**LOCUS** A68204 1239 bp DNA linear PAT 06-MAY-1999  
**DEFINITION** Sequence 2 from Patent WO9746690.  
**ACCESSION** A68204  
**VERSION** A68204.1 GI:4759372  
**KEYWORDS**  
**SOURCE** tomato.  
**ORGANISM** Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; eusterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.  
**REFERENCE** 1 (bases 1 to 1239)  
**AUTHORS** Drake, C.R., Bird, C.R. and Schuch, W.W.  
**TITLE** ENHANCEMENT OF GENE EXPRESSION  
**JOURNAL** Patent: WO 9746690-A 2 11-DEC-1997;  
 ZENECA LTD (GB)  
**FEATURES** Location/Qualifiers  
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 Pred. No.: 3,42e-142 Length: 1239  
 Score: 1750.00 Matches: 344  
 Percent Similarity: 86.84% Conservative: 32  
 Best Local Similarity: 79.45% Mismatches: 33  
 Query Match: 77.09% Indels: 24  
 DB: 6 Gaps: 3  
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 Db 709 TACCTTTATTTATTATGTTGCTGTGACGTTGGTGTGATGAGTGTTCCAATATGGGT 768  
 QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302  
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 Db 769 ATCGCCCTGAATCAAGGCAACACAGAGCGGTATATATGCTGCTTTGGCTCTGGGG 828  
 QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArg 322  
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 Db 829 ATCGCAATCAATTAACATACATCTCAGAGATGTTGGAGAAGATGCCAGAGAGGAGA 888  
 QY 323 ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342  
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 Db 889 GTCTACTTGGCTCAAGATGAATTAGCACAGCAGGTCTATCCGATGAAGATATATTGCT 948  
 QY 343 GlyArgValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362  
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 QY 383 LeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402  
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 QY 403 AsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla 422  
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 Db 1129 AACTTCACAAAGAGAGCATATGTGAGCAAAATCAAGAAAGTTGATTGCTACCTATTGCA 1188  
 QY 423 TyrAlaLysSerLeuValProProAsnArgThrSerSer 435  
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 Db 1189 TATGCAAAATCTCTTGTGCTCTCTACAAAACCTGCCTCT 1227  
**RESULT 4**  
**LOCUS** ARI56064 1239 bp DNA linear PAT 08-AUG-2001  
**DEFINITION** Sequence 2 from patent US 6239331.  
**ACCESSION** ARI56064  
**VERSION** ARI56064.1 GI:15124117  
**KEYWORDS**  
**SOURCE** Unknown.  
**ORGANISM** Unknown.  
 Unclassified.  
**REFERENCE** 1 (bases 1 to 1239)  
**AUTHORS** Drake, C.Rachel., Bird, C.Roger. and Schuch, W.Walter.  
**TITLE** Enhancement of tomato phytoene synthase gene expression with a modified DNA  
**JOURNAL** Patent: US 6239331-A 2 29-MAY-2001;  
**FEATURES** Location/Qualifiers  
 source  
 1..1239  
 /organism="unknown"  
**BASE COUNT** 377 a 207 c 317 g 338 t  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 3,42e-142 Length: 1239

[illegible]

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QY 43 AspArgAsnLeuMetTrpAsnGlyArgGlyLeuLysGlyArgGlnArgTrpAsnPhe 62
Db 106 CATAGGATTTGGTCCCATGAGAGATCAATAGAGT-----144
QY 63 GlySerLeuLeuAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
Db 145 -----GGTGGAAAGCAACTAATAATGGA 168
QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
Db 169 CGGAAATTTCTAGCGGTGCTATATTTGGCTACTCATCTGGAGAACGGAGATGACA 228
QY 103 SerGluLysValTrpAspValValLeuLysGlnAlaAlaLeuValLysArgGlnLeu 122
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QY 123 ArgSerThrAspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeu 142
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QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaTrpAlaTrpAlaTrpValTrp 182
Db 409 TTAGGAACTATGCTATGATCTCCGAGAGAGAGGCGCTATCTGGGCAATATATGATGG 468
QY 183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202
Db 469 TGCAGAGAACACATGACATGTTGATGGCCCAACGATCATATATACCCCGGCGAGCC 528
QY 203 LeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
Db 529 TTAGATAGGTGGGAAATAGGCTAGAGATGTTTCAATGGGCGGCAATTTGACATGCTC 588
QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
Db 589 GATGGTGTCTTGGCCATACAGTTTCTACTTCCAGTTGATATTCAGCCATTCAGAGAT 648
QY 243 MetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeu 262
Db 649 ATGATTGAAGCAATGCGTATGGACTTGAGAAATCGAGATAACAAACATCGACGAACTA 708
QY 263 TyrLeuTyrCysTyrTrpValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
Db 709 TACCTTTATTTATTTATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768
QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302
Db 769 ATGCCCCCTGAATCAAGGCAACACAGAGAGCGTATATATCTCTTGGCTGTGGGG 828
QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArg 322
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Db 889 GTCTACTTGCCTCAAGATGAATTAGCACAGGCGAGGTCTATCCGATGAAGATATATTTGCT 948
QY 343 GlyArgValThrAspLysTrpArgAsnPheMetLysGlnIleGlnArgAlaArgLys 362
Db 949 GGAAGGTGACCCATAAATGGAGAAATCTTTATGAAGAAACAAATACATAGGGCAAGAAAG 1008
QY 363 PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal 382
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QY 403 AsnPheThrArgArgAlaTrpValSerLysProLysLysLeuLeuThrLeuProIleAla 422
Db 1129 AACTTCACAAAGAGACATATGTGACAAATCAAGAAGTTGATTGCATTACCTATTGCA 1188
QY 423 TyrAlaLysSerLeuValProProAsnArgThrSerSer 435
Db 1189 TATGCAAAATCTCTTGTGCTCTCTCAAAAAGTGCCTCT 1227
RESULT 6
A68203
LOCUS A68203 1239 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 1 from Patent WO9746690.
ACCESSION A68203
VERSION A68203.1 GI:4759371
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1239)
AUTHORS Drake, C.R., Bird, C.R. and Schuch, W.W.
TITLE ENHANCEMENT OF GENE EXPRESSION
JOURNAL Patent: WO 9746690-A 1 11-DEC-1997;
ZENECA LTD (GB)
FEATURES
Location/Qualifiers
Source 1..1239
/organism="unidentified"
/isolate="SYNTHETIC DNA"
/db_xref="taxon:32644"
BASE COUNT 343 a 247 c 320 g 329 t
ORIGIN
Alignment Scores:
Pred. No.: 1..13e-141 Length: 1239
Score: 1744.00 Matches: 343
Percent Similarity: 86.61% Conservative: 32
Best Local Similarity: 79.21% Mismatches: 34
Query Match: 76.83% Indels: 24
DB: 6 Gaps: 3
US-09-847-081B-2 (1-440) x A68203 (1-1239)
QY 3 MetSerValAlaLeuLeuTrpValSerProThrSerGluValSerAsnGlyThrGly 22
Db 1 ATGAGCGTGGCAGCTTCTTTGGGTGGTGAGCCCA---TGCATGTGAGTAACGGCAGCTCA 57
QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
Db 58 TTTATGGAGAGTGTGAGAGAGGTAATAGATTCTTCGACAGTTCT-----CGT 105
QY 43 AspArgAsnLeuMetTrpAsnGlyArgGlyLeuLysGlyGlyArgGlnArgTrpAsnPhe 62
Db 106 CACCGTAACTCTGTTAGTAACAGCAACGATATAACAGGGGA-----144
QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
Db 145 -----GGAGTTAAACAGACAACACCGT 168
QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
Db 169 AGAAAGTTCTCAGTTAGATCAGCAATCTTGGCAACACCTAGCGGTGAGAGCACTATGACT 228
QY 103 SerGluLysValTrpAspValValLeuLysGlnAlaAlaLeuValLysArgGlnLeu 122
Db 229 AGCGAGCAATAGTGTACGACGCTGCTACTTCTGCAAGCTGCAGTAGTTAAACGCTCAGTTA 288
QY 123 ArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeu 142
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QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrAlaLysThrValTyr 182  
DB 409 TTGGGTACCATGTTGATGACACAGAGAGCGCTGTCGATATGGCTATTTACGTTGG 468  
QY 183 CysArgArgThrAspGluValAspGlyProAsnAlaSerHisIleThrProGlnAla 202  
DB 469 TGTAGCGTACTGACGAGTTAGTGACGAGCACTTAATGCTAGTATACATACACCGCTGT 528  
QY 203 LeuAspArgThrProGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222  
DB 529 CTGACAGATGGGAGAACCGTTTGGAGGACGTTTAAACGCGACCTTTTCGATATGTTG 588  
QY 223 AspAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgasp 242  
DB 589 GACGGAGCACTTAGTGACACTGTAGCAATTTCCCTGTGGACATCCAACTTTTCGGGAC 648  
QY 243 MetIleGluGlyMetArgMetAspLeuThrLysSerArgTyrLysThrPheAspGluLeu 262  
DB 649 ATGATCGAGGCGATGAGATGATCTCGTAAGTCTCGTTATAAGAAATTTTCATGATGTTG 708  
QY 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282  
DB 709 TATTTGTACTGTACTACTGTGCGAGAACCGTGGGCGCTTATCTAGTGCCTATCATGGGA 768  
QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeuAlaLeuGly 302  
DB 769 ATGCACAGAGATGAACTACTACTGATCTGTTACCGCGACACTACATAGGT 828  
QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArg 322  
DB 829 ATAGCTAACAGCTTACAAATATCTTGGGAGCGTGGGTGAGGACGACAGTGGGCTGT 888  
QY 323 ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342  
DB 889 GTGATCTCCACAGAGAGCTGCTCAAGCTGGATTGAGTGACGAGGACATTTTCGCA 948  
QY 343 GlyArgValThrAspLysThrArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362  
DB 949 GTGCGTGTACAGACAGTGGAGGATTTTCATGAAAGACCATTCACCGTCTCGTAAA 1008  
QY 363 PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyrProVal 382  
DB 1009 TTTTTCGAGAACTGAAAGGAGTACTGAGCTTCTAGTGCATCAAGTTTCCAGTT 1068  
QY 383 LeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402  
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QY 403 AsnPheThrArgArgAlaTyrValSerLysProLysLysLysLeuThrLeuProIleAla 422  
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QY 423 TyrAlaLysSerLeuValProProAsnArgThrSerSer 435  
DB 1189 TAGCTAAGAGCTTGGTCCACCACTAAGACAGCTAGC 1227

RESULT 7  
ARL56063  
LOCUS ARL56063 1239 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 1 from patent US 6239331.  
ACCESSION ARL56063  
VERSION ARL56063.1 GI:15124116

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 1239)  
AUTHORS Drake, C. Rachel., Bird, C. Roger. and Schuch, W. Walter.  
TITLE Enhancement of tomato phytoene synthase gene expression with a

modified DNA  
JOURNAL Patent: US 6239331-A 1 29-MAY-2001:  
FEATURES Location/Qualifiers

source 1..1239  
/organism="unknown"  
BASE COUNT 343 a 247 c 320 g 329 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1..13e-141 Length: 1239  
Score: 1744.00 Matches: 343  
Percent Similarity: 86.61% Conservative: 32  
Best Local Similarity: 79.21% Mismatches: 34  
Query Match: 76.83% Indels: 24  
DB: 6 Gaps: 3

US-09-847-081B-2 (1-440) x ARL56063 (1-1239)

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QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42  
DB 58 TTTATGGAGAGTGTGAGAGAAGGTAATAGATTCTTCGACAGTTCT-----CGT 105  
QY 43 AspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGlnArgTyrAsnPhe 62  
DB 106 CACCGTAACTTGTGTAGTAACGACGTATAACAGGGGA----- 144  
QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82  
DB 145 -----GGAGCTAAACAGACAAACACGCT 168  
QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102  
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DB 229 ACGGACCAATGGTGTACGCGCTGCTACTTCGTCAAGCTGCACCTAGTTAAACGCTCAGTTA 288  
QY 123 ArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeuGlyLeu 142  
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QY 143 LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyr 162  
DB 349 CTTTCTGAGGCTTACGACAGATGCGGAGAGGTTTGGCAGAAATACGCTAAACCTTCAAT 408  
QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrAlaIleTyrValTyr 182  
DB 409 TTGGGTACCATGTTGATGACACAGACAGAGCGCTGTCGCAATATGGCTATTTACGTTGG 468  
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DB 469 TGTAGCGTACTGACGAGTTAGTGACGAGCACTTAATGCTAGTTACATACACCGCTGCT 528  
QY 203 LeuAspArgThrGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222  
DB 529 CTGACAGATGGGAGAACCGTTTGGAGGACGTTTAAACGCGACCTTTTCGATATGTTG 588  
QY 223 AspAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgasp 242  
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QY 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282  
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DB 949 GGTGCTGTACAGCAAGTGGAGGATTTTCATGAAAAGCAGATCACCGTGTCTGATAA 1008
QY 363 PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyrProVal 382
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QY 383 LeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402
DB 1069 TGGCCAGCCTTGTGCTCTATAGAGATTTTGGACGAAATCGAGCGCTAACGATTATAAT 1128
QY 403 AsnPheThrArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla 422
DB 1129 AATTTACTAACGCTGCTTACGTTTCTAAGAGCAAAATCTTATCGCTCTTCCAAATCGCT 1188
QY 423 TyrAlaLysSerLeuValProAsnArgThrSerSer 435
DB 1189 TAGCTAAGAGCTGTGTTCCACCACTAAGACAGCTAGC 1227

RESULT 8
BD005485 1239 bp DNA linear PAT 31-JAN-2002
LOCUS Enhancement of gene expression.
DEFINITION BD005485
ACCESSION BD005485
VERSION BD005485.1 GI:18633856
KEYWORDS JP 2001501810-A/1.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1239)
AUTHORS Drake,C.R., Bird,C.R. and Schuch,W.W.
TITLE Enhancement of gene expression
JOURNAL Patent: JP 2001501810-A 1 13-FEB-2001;
ZENECA LTD
COMMENT OS Unidentified
PN JP 2001501810-A/1
PD 13-FEB-2001
PF 23-MAY-1997 JP 1998500302
PR 07-JUN-1996 GB 9611981.3
PI CAROLINE RACHEL DRAKE, COLIN ROGER BIRD, WOLFGANG WALTER SCHUCH
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BASE COUNT 343 a 247 c 320 g 329 t
ORIGIN

Alignment Scores:
Pred. No.: 1,13e-141 Length: 1239
Score: 1744.00 Matches: 343
Percent Similarity: 86.61% Conservative: 32
Best Local Similarity: 79.21% Mismatches: 34
Query Match: 76.83% Indels: 24

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DB: 6 Gaps: 3

US-09-847-081B-2 (1-440) x BD005485 (1-1239)

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DB 58 TTTATGGAGAGTGTGAGAGAAGGTAATAGATTCTTCACAGTTCT-----CGT 105

QY 43 AspArgAsnLeuMetTyrPasnGlyArgIleLysLysGlyArgGlnArgTyrAsnPhe 62

DB 106 CACCGTAACCTTGTGTAGTAACGAACGTATAAACAGGGGA----- 144

QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82

DB 145 -----GGAGGTAACACAGACAACACCGGT 168

QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102

DB 169 AGAAAGTCTCTCAGTTAGATCAGCAATCTTGCACACCTAGCGGTGAGAACATATGACT 228

QY 103 SerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArgGlnLeu 122

DB 229 AGCGACAATGTGTACGACGCTGCTACTTCGTCAAGCTGCACCTAGTTAAACGTCAGTTA 288

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DB 289 CGTAGTACTAACCAACTTGGAGTTAAACCTGACATTCCTGGAACCTTGGACTT 348

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QY 243 MetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPheAspGluLeu 262

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QY 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282

DB 709 TATTTGCTACTGCTACTACGTGCGAGGAACCGTGGGCGCTTATGTCAGTGCCTATCATGGGA 768

QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302

DB 769 ATTGCACGAGAGTAAGCTACTACTGTAATCTGTTTACACCGCAGCAGTAGCATTAGGT 828

QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArg 322

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QY 323 ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342

DB 889 GTGTATCTCCACAGGACGAGCTCGCTCAAGCTGGATTGAGTGACGAGGACATTTTCGCA 948

QY 343 GlyArgValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362



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Db 949 GGTCTGTACAGCAAGTGGAGGATTTTCATGAAAGACAGATTCACCGTCTCGTAAA 1008
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Db 1009 TTTTTCGAGAGCTGAAAGGAGTACTAGCTTCTAGTGCATCAAGGTTTCCAGTT 1068
QY 383 LeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402
Db 1069 TGGGCCAGCCTGTGCTCTATAGAAGATTTTGGACGAATCGAGGCTAAGGATTATAAT 1128
QY 403 AsnPheThrArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla 422
Db 1129 AATTTTACTAAGCGTCTAGCTTCTAAGAGCAAAACATATGCTCTTCCAATCGT 1188
QY 423 TyrAlaLysSerLeuValProAsnArgThrSerSer 435
Db 1189 TACGCTAAGAGCTTGGTTCCACCACTAAGACAGCTAGC 1227

RESULT 9
LERIPE
LOCUS LERIPE 1614 bp mRNA linear PLN 11-MAY-1995
DEFINITION Tomato fruit ripening specific mRNA.
ACCESSION Y00521
VERSION Y00521.1 GI:19340
KEYWORDS unidentified reading frame.
SOURCE Lycopersicon esculentum.
ORGANISM Lycopersicon esculentum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 1614)
AUTHORS Bird,C.R.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1987) Bird C.R., Imperial chemical industries
PLC, plant biotechnology group, Po Box 11, The Health, Runcorn,
Cheshire, WA7 4QE, U.K.
2 (bases 1 to 1614)
AUTHORS Ray,J., Bird,C., Maunders,M., Grierson,D. and Schuch,W.
TITLE Sequence of pTOM5, a ripening related cDNA from tomato
JOURNAL Nucleic Acids Res. 15 (24), 10587 (1987)
MEDLINE 88096591
PUBMED 3637037
FEATURES
source
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/strain="Mill."
/cultivar="Alisa Craig"
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702..710
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BASE COUNT 515 a 241 c 388 g 470 t
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Alignment Scores:
Pred. No.: 1,43e-140 Length: 1614
Score: 1733.00 Matches: 346
Percent Similarity: 85.68% Conservative: 31
Best Local Similarity: 78.64% Mismatches: 36
Query Match: 76.34% Indels: 27
DB: 8 Gaps: 4
US-09-847-081b-2 (1-440) x LERIPE (1-1614)
QY 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly 20
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QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
Db 252 ACAAGTTTCATGGAAATCATGTCGGGAGGAAACCGTTTTTTTGTGATTCATCG 302
QY 41 AlaArgAspAlaGlnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGlnArgTyr 60
Db 303 ---AGGCATAGGAATTTGGTGTCCCAATGAGAGAAACAATAGAGGT----- 344
QY 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
Db 345 -----GGTGAAAGCAAACTAAT 362
QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
Db 363 AATGACCGGAAATTTTCTGTAGCGTCTGCTATTTTGGTACTCCATCTCGAGAACGAGC 422
QY 101 ValSerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArg 120
Db 423 ATGACATCGGAACACATGCTCTATGTTGTTGAGCAGCAGCCCTTGTGAAGAGG 482
QY 121 GlnLeuArgSerThrAspLeuValLysProAspIleValValProGlyAsnLeu 140
Db 483 CAACTGAGATCTACCAATGAGTTAGAAGTGAAGCCGGATATACCTATTCCGGGAATTTG 542
QY 141 GlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThr 160
Db 543 GGCTTTGTCAGTGAAGCATATGATAGTGTGTGTAAGTATGTCAGAGATGATCAAGAGC 602
QY 161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPheAlaIleTyr 180
Db 603 TTTAACTTAGGAACATGCTAATGACTCCGAGAGAAGAGGGCTATCTGGGCAATATAT 652
QY 181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
Db 663 GTATGGTCAGAGAACAAGATCAACTTGTGTATGGCCCAACGATCATATATACCCCG 722
QY 201 GlnAlaLeuAspArgTyrGluThrArgLeuGluAspIlePheSerGlyArgPropheAsp 220
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QY 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
Db 783 ATGCTCGATGGGTGTTGTCGATACAGTTTCTTAACCTTCCAGTTGATATTCAGCCATTC 842
QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAsp 260
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QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
Db 903 GAACATATACCTTTATTTGTTATTATGTTGCTGCTACGGTTGGTGTGATGAGTGTCCAATT 962
QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeuAla 300
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QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
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QY 321 GlyArgValLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
    |||...|||
DB 1083 GGAAGAGTCTACTGCCTCAAGATCAATAGACAGGAGGCTATCCGATGAAGATATA 1142
QY 341 PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysGlyGlnIleGlnArgAla 360
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DB 1143 TTGTGGAAGGTCACCATTAATGGAGATCTTTATGAGAAACAATACATAGGCA 1202
QY 361 ArgLysPheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrp 380
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DB 1203 AGAAAGTCTTGTGATGAGCAGAGAAGCGTGACAGAAATGAGTCACTAGTATGATTC 1262
QY 381 ProValLeuThrAlaLeuLeuLeuTrpArgLysIleLeuAspGluIleGluAlaAsnAsp 400
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DB 1263 CCTGTATGGGCATCTTGTGCTGTACCGCAAAATAGATGAGATTGAACCCATGAC 1322
QY 401 TyrAsnAsnPheThrArgArgAlaTrpValSerLysProLys-LysLeuLeuThrLeuPr 420
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DB 1323 TACAACAACCTCACAAAGAGAGCATATGTGACAAATCAAGCAAGTTGATTGCATTACC 1382
QY 420 OrlaAlaTrpAlaLysSerLeuValProAsnArgThrSerSerProLeuAlaLys 439
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DB 1383 TATTGCATATGCAAAATCTCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1434

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## RESULT 10

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A21360 LOCUS A21360 1646 bp mRNA linear PAT 06-JUN-1994
DEFINITION L-esculentum PTOM5 mRNA.
ACCESSION A21360
VERSION A21360.1 GI:512395

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## KEYWORDS

SOURCE Lycopersicon esculentum.

## ORGANISM

Lycopersicon esculentum.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.

## FEATURES

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polyA\_site 529 a 249 c 388 g 480 t

## BASE COUNT

## ORIGIN

## Alignment Scores:

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Pred. No.: 1,78e-140 Length: 1646
Score: 1732.00 Matches: 346
Percent Similarity: 85.68% Conservative: 31
Best Local Similarity: 78.64% Mismatches: 36
Query Match: 76.30% Indels: 27

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DB 195 CTCACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
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DB 252 ACAAGTTTCATGGAATCAGTCGCGGAGGAAACCGTTTTTTTGTATCATCG----- 302
QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyClyArgGlnArgTrp 60
    |||...|||
DB 303 ---AGGCATAGGAATTTGGTGCCATAGAGAATCAATAGAGGT----- 344
QY 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgTrpGlu 80
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DB 345 -----GGTGGAAAGCAAACTAAT 362
QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
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DB 363 AATGACGCGAAATTTTCTGACGGTCTGCTATTTTGGTACTCCATCTCGAGAACGACG 422
QY 101 ValSerSerGluLysValTrpAspValValLeuLysGlnAlaLeuValLysArg 120
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DB 423 ATGACATCGGAACAGATGGTCTATGATGGTGTGGAGCGAGCGCTGGTGAAGAGG 482
QY 121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeu 140
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QY 161 PheTrpLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTrp 180
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QY 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp 220
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QY 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
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DB 903 GAACTATACCTTTATTGTTATTATGTTGCTGACGTTGGTGGTGGTGGTGGTGGTGGTGGT 962
QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTrpAsnAlaAlaLeuAla 300
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DB 1023 CTGGGATCGCAATCAATTAACATACATACATGAGATGTTGGAGAGATGCCAGAAGA 1082
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QY 401 TyrAsnAspPheThrArgAlaTyrValSerLysProLys-LysLeuLeuThrLeuPr 420
Db 1323 TACAACACTTTCACAAAGAGACATATGTGACAAATCAAGCAAGTGAATGCAATGAC 1382
QY 420 orlealatyAlaLysSerLeuValProProAsnArgThrSerProLeuAlaLys 439
Db 1383 TATTGCATATGCAAAATCTTTGCTCCT-----ACAAACTGCCCTCTCTTCAA 1434

RESULT 11
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LOCUS AR007503 1646 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5750865.
ACCESSION AR007503
VERSION AR007503.1 GI:3966987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1646)
AUTHORS Bird,C.Roger., Grierson,D. and Schuch,W.Walter.
TITLE Process for modifying the production of carotenoids in plants, and
DNA, constructs and cells therefor
JOURNAL Patent: US 5750865-A 2 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..1646
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BASE COUNT 529 a 249 c 388 g 480 t
ORIGIN

Alignment Scores:
Pred. No.: 1,78e-140 Length: 1646
Score: 1732.00 Matches: 346
Percent Similarity: 85.68% Conservative: 31
Best Local Similarity: 78.64% Mismatches: 36
Query Match: 76.30% Indels: 27
DB: 6 Gaps: 4

US-09-847-081B-2 (1-440) x AR007503 (1-1646)
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Db 252 ACAAGTTTCATGAATCAGTCGCGGAGGAAACCGTTTTTTTGAATCATCG----- 302
QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGlnArgTrp 60
Db 303 ---AGCATAGGAATTTGGTGTCCAATGAGAGAATCAATAGAGGT----- 344
QY 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
Db 345 -----GGTGGAAAGCAAACTAAT 362
QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
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QY 141 GlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThr 160
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QY 161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyr 180
Db 603 TTTAACTTAGGAACATGCTAATGACTCCCGAGAGAAAGGGCTATCTCGGCAATATAT 662
QY 181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
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Db 1143 TTTGCTGGAAGGGTGACCGATAAATGGAGAACTCTTTATGAAGAAACAAATACATAGGCA 1202
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Db 1323 TACAACACTTTCACAAAGAGACATATGTGACAAATCAAGCAAGTGAATGCAATGAC 1382
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RESULT 12
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LOCUS LERYGTOM5 1355 bp mRNA linear PLN 02-AUG-1993
DEFINITION L.esculentum (ry mutant) G10M5 mRNA for mutant phytoene synthase.
ACCESSION X67144.1
VERSION X67144.1 GI:19346
KEYWORDS G10M5 gene; mutant; phytoene synthase.
SOURCE Lycopersicon esculentum.

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ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; eusterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE 1 (bases 1 to 1355)  
AUTHORS Fray, R.G.  
TITLE Direct Submission  
JOURNAL Submitted (01-JUL-1992) R.G. Fray, University of Nottingham, School  
of Agriculture, Sutton Bonington, Loughborough, Leicestershire LE12  
5RD, UK  
REFERENCE 2 (bases 1 to 1355)  
AUTHORS Fray, R.G. and Grierson, D.  
TITLE Identification and genetic analysis of normal and mutant phytoene  
synthase genes of tomato by sequencing, complementation and  
co-suppression  
JOURNAL Plant Mol. Biol. 22 (4), 589-602 (1993)  
MEDLINE 93344508  
PUBMED 8343597

## FEATURES

## Location/Qualifiers

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1171..1335

variation 412 a 223 c 354 g 366 t  
BASE COUNT  
ORIGIN

Alignment Scores:  
Pred. No.: 4,75e-135 Length: 1355  
Score: 1668.00 Matches: 329  
Percent Similarity: 86.27% Conservative: 29  
Best Local Similarity: 79.28% Mismatches: 33  
Query Match: 73.48% Indels: 24  
DB: 8 Gaps: 3

US-09-847-081b-2 (1-440) x LERYGTOM5 (1-1355)

QY 2 SerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThr 21  
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QY 22 GlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAla 41  
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QY 42 ArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuLysGlyGlyArgGlnArgTrpAsn 61  
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Db 111 AGGATAGGAATTTGGTGTCCATGAGAAATCAATAGAGGT----- 152  
QY 62 PheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLys 81

Db 153 -----|||||  
QY 82 GlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrVal 101  
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Db 174 GGACGGAAATTTTCTGTACGGTCTGCTATTTTGGCTACTCCATCTGGAGAAGCAGCATG 233  
QY 102 SerSerGluLysLysValTyrAspValValLeuLysGlnAlaAlaLeuValLysArgGln 121  
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QY 122 LeuArgSerThrAspAspLeuGluValLysProAspLeuValProGlyAsnLeuGly 141  
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Db 294 CTGAGATCTACCAATGAGTTAGAGTGAAGCCGATATCTATTCGGGGAAATTTGGGC 353  
QY 142 LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhe 161  
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Db 474 TGGTGACAGAAGAACAGATGAACCTTGTGATGCCCAACACATCATATATACCCCGCA 533  
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Db 594 CTCGATGGTGTGTCGATACAGATTTCTAACTTTCCAGTTGATATTCAGCCATTGACA 653  
QY 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu 261  
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Db 714 CTATACCTTTATTGTTATTATGTTGCTGTGACGTTGGTGGTGTGAGTGTGTTCCAAATTATG 773  
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Db 774 GGTATCGCCCTGAATCAAAAGGCAACACAGAGAGCGGTATATATGCTGCTTTGGCTCTG 833  
QY 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGly 321  
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Db 954 GCTGGAAGGGTGAACCAATTAATGGAATCTTTATGAAGAAACAAATACATAGGCGCAAGA 1013  
QY 362 LysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpPro 381  
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Db 1014 AAGTCTTTGATGAGCAGAGAAGCGGTGACAGAAATGAGCTCAGCTAGTAGATTCCT 1073  
QY 382 ValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyr 401  
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Db 1074 GTATGGGCTCTTTGCTGTGTACCGCAAAATACTAGATCAGATTTGAAGCAATGACTAC 1133  
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AP220218



**LOCUS** AB037975 1689 bp mRNA linear PLN 25-NOV-2000  
**DEFINITION** Citrus unshiu mRNA for phytoene synthase, complete cds.  
**ACCESSION** AB037975  
**VERSION** AB037975.1 GI:11344506  
**KEYWORDS** phytoene synthase.  
**SOURCE** Citrus unshiu (cultivar:Satsuma mandarin) mature stage pulp cDNA to mRNA.  
**ORGANISM** Citrus unshiu  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.  
**REFERENCE** 1 (sites)  
**AUTHORS** Ikoma,Y., Komatsu,A., Kita,M., Ogawa,K., Omura,M., Yano,M. and Moriguchi,T.  
**TITLE** Expression of a phytoene synthase gene and characteristic carotenoid accumulation during citrus fruit development  
**JOURNAL** Physiol. Plantarum 111, 232-238 (2001)  
**REFERENCE** 2 (bases 1 to 1689)  
**AUTHORS** Moriguchi,T.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (04-FEB-2000) Takaya Moriguchi, National Institute of Fruit Tree Science, Department of Research Planning and Coordination; 2-1 Fujimoto, Tsukuba, Ibaraki 305-8605, Japan (E-mail: takaya@fruit.affrc.go.jp, Tel:81-298-38-6416, Fax:81-298-38-6437)  
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 ORIGIN

**Alignment Scores:**  
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 Score: 1626.00 Matches: 327  
 Percent Similarity: 82.61% Conservative: 34  
 Best Local Similarity: 74.83% Mismatches: 64  
 Query Match: 71.63% Indels: 12  
 DB: 8 Gaps: 4

US-09-847-081b-2 (1-440) x AB037975 (1-1689)

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 Db 176 AGCATGCTGTACATGCTGTGGTGTATCATCACTAACTACAAATGTCTCAATGGCTC 235  
 Qy 22 GlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerArgPheLeu--- 40  
 Db 236 GGGTCTCGATCAGTTCGAGAGAAACAGGCGTGTATTATCATCAAGATTCTCTTAC 295  
 Qy 41 ---AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLys-----GlyGly 56  
 Db 296 CAACATCAACCCGGACTGTGTGTTAAATCTAGACCTAAGCAGATTAAATATAGTAAT 355  
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## RESULT 15

AF152892 1773 bp mRNA linear PLN 04-APR-2001  
 LOCUS Citrus x paradisi phytoene synthase mRNA, complete cds.  
 DEFINITION AF152892  
 ACCESSION AF152892  
 VERSION AF152892.2 GI:13542331  
 KEYWORDS Citrus x paradisi.  
 SOURCE Citrus x paradisi.  
 ORGANISM Citrus x paradisi.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

## REFERENCE

AUTHORS Costa, M.C., Moreira, C.D., Melton, J.R., Otoni, W.C. and Moore, G.A.  
 TITLE Developmental expression of carotenoid genes in Citrus  
 JOURNAL Unpublished  
 REFERENCE 1 (bases 1 to 1773)  
 AUTHORS Costa, M.C., Moreira, C.D., Melton, J.R., Otoni, W.C. and Moore, G.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-MAY-1999) Horticultural Sciences, University of  
 Florida, 1301 Field Hall, Gainesville, FL 32611, USA  
 REFERENCE 2 (bases 1 to 1773)  
 AUTHORS Costa, M.C., Moreira, C.D., Melton, J.R., Otoni, W.C. and Moore, G.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-APR-2001) Horticultural Sciences, University of  
 Florida, 1301 Field Hall, Gainesville, FL 32611, USA  
 REMARK Sequence update by submitter  
 COMMENT On Apr 4, 2001 this sequence version replaced gi:5020351.  
 FEATURES Location/Qualifiers

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 ORIGIN

## Alignment Scores:

Pred. No.: 1..55e-129 Length: 1773  
 Score: 1606.00 Matches: 324  
 Percent Similarity: 82.1% Conservative: 35  
 Best Local Similarity: 74.14% Mismatches: 66  
 Query Match: 70.75% Indels: 12  
 DB: 8 Gaps: 4

US-09-847-081B-2 (1-440) x AF152892 (1-1773)

QY 2 SerMetSerValAlaLeuLeuValSerProThrSerGluValSerAsnGlyThr 21  
 DB 248 AGCATGCTGTACATGCTGGGTGTATCACCTAACTCAATGTCCCAATTGCTTC 307  
 QY 22 GlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerArgPheLeu--- 40  
 DB 308 GGGTTCGTGATTCAGTTCGAGAGGAAACAGCGCTTTTATTCATCAGATTTCTTAC 367  
 QY 41 ---AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLys-----GlyGly 56  
 DB 368 CAACATCAACACCGGCACTGCTGTGTAAATCTGACACCTTAAGCAGTTAATAAGTAAT 427  
 QY 57 ArgGlnArgTrpAsnGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGly 76  
 DB 428 AAGCAGAGAGGAGNATCTTATCTCTTAGATACAGATTTGAGGCATCCTTCG----- 478

QY 77 SerArgThrGluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAla 96  
 DB 479 -----TCATCTGGATTCGACTTGCCTGAAATATCATGTATGTTGCTACACTGCT 529  
 QY 97 GlyGluMetThrValSerSerGluLysLysValTyrAspValValLeuLysGlnAlaAla 116  
 DB 530 GGAGAAGTGGCCATGCTCTTCAAGAAGAAATGGTTTACAATGTTGCTCAAGCAGGAGCC 589  
 QY 117 LeuValLysArgGlnLeuArgSer---ThrAspAspLeuValLysProAspIleVal 135  
 DB 590 TTGGTTAATAAGCAACCAAGTGGGTACTCGTATCTTGCATGTGAACCCAGATATGCT 649  
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